OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/044,807

DATE: 01/30/2002
TIME: 15:44:46

Input Set : A:\LEX-0298-USA SEQLIST.txt
Output Set: N:\CRF3\01302002\J044807.raw

ENTERED

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      4 <110> APPLICANT: Yu, Xuanchuan
      5       Turner, C. Alexander Jr.
      7 <120> TITLE OF INVENTION: Novel Human Protease and Polynucleotides Encoding the Same
      9 <130> FILE REFERENCE: LEX-0298-USA
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/044,807
C--> 11 <141> CURRENT FILING DATE: 2002-01-11
     11 <150> PRIOR APPLICATION NUMBER: US 60/261,684
     12 <151> PRIOR FILING DATE: 2001-01-12
     14 <160> NUMBER OF SEQ ID NOS: 2
     16 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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     19 <211> LENGTH: 5289
     20 <212> TYPE: DNA
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     26 ccatggagtg aatgctcacg cacctgcggg ggtggggcct cctactctct gaggcgctgc     180
     27 ctgagcagca agagctgtga aggaagaaat atccgataca gaacatgcag taatgtggac     240
     28 tgcccaccag aagcaggtga tttccgagct cagcaatgct cagctcataa tgatgtcaag     300
     29 caccatggcc agttttatga atggcttcct gtgtctaatg accctgacaa cccatgttca     360
     30 ctcaagtgcc aagccaaagg aacaaccctg gttgttgaac tagcacctaa ggtcttagat     420
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     35 ggtcctgatc acttatatct ggaaaccaaa accctccagg ggactaaagg tgaaaacagt     720
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     40 tcggctgagt gctacgatct gaggagcaac cgtgtggttg ctgaccaata ctgtcactat    1020
     41 tacccagaga acatcaaacc caaacccaag cttcaggagt gcaacttgga tccttgtcca    1080
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52 gacctgccta ttgacgagtg tgaagggccc aagccagcat cccagcgtgc ctgttatgca 1740
53 ggcccatgca gcggggaaat tcctgagttc aacccagacg agacagatgg gctctttggt 1800
54 ggcctgcagg atttcgacga gctgtatgac tgggagtatg aggggttcac caagtgctcc 1860
55 gagtcctgtg gaggaggtgt ccaggaggct gtggtgagct gcttgaacaa acagactcgg 1920
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60 caagcttgta accgctttaa ttgccccca gcctggtacc ctgcacagtg gcagccgtgt 2220
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62 gatggcagct tcctggagct tcctgagacc ttctgttcag cttcaaaacc tgcctgccag 2340
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64 tccacaagct gcggggaagg cacccagact cgaagcgcca tttgccgaaa gatgctgaaa 2460
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66 atcaggccct gtatgctggc aacctgtgca aggcccgggc ggccatccac gaagcacagc 2580
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68 ttcgtggtgg ggggcttcgc ctacctgctc cccaagacgg cggtggtgct gcgctgcccg 2700
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103 tccacccctg tgtccaatga catgtgcacc caggtcgcca agcggcctgt ggacacccag    4800
104 gcctgtaacc agcagctgtg tgtggagtgg gccttctcca gctggggcca gtgcaatggg    4860
105 ccttgcatcg ggcctcacct agctgtgcaa cacagacaag tcttctgcca gacacgggat    4920
106 ggcatcacct taccatcaga gcagtgcagt gctcttccga ggcctgtgag cacccagaac    4980
107 tgctggtcag aggcctgcag tgtacactgg agagtcagcc tgtggaccct gtgcacagct    5040
108 acctgtggca actacggctt ccagtcccgg cgtgtggagt gtgtgcatgc ccgcaccaac    5100
109 aaggcagtgc ctgagcacct gtgctcctgg gggccccggc ctgccaactg gcagcgctgc    5160
110 aacatcaccc catgtgaaaa catggagtgc agagacacca ccaggtactg cgagaaggtg    5220
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112 aaagcgtga                                                           5289
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117 <211> LENGTH: 1762
118 <212> TYPE: PRT
119 <213> ORGANISM: homo sapiens
121 <400> SEQUENCE: 2
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125             20                  25                  30
126 Asp Gly Leu Trp Asp Ala Trp Gly Pro Trp Ser Glu Cys Ser Arg Thr
127         35                  40                  45
128 Cys Gly Gly Gly Ala Ser Tyr Ser Leu Arg Arg Cys Leu Ser Ser Lys
129     50                  55                  60
130 Ser Cys Glu Gly Arg Asn Ile Arg Tyr Arg Thr Cys Ser Asn Val Asp
131 65                  70                  75                  80
132 Cys Pro Pro Glu Ala Gly Asp Phe Arg Ala Gln Gln Cys Ser Ala His
133                 85                  90                  95
134 Asn Asp Val Lys His His Gly Gln Phe Tyr Glu Trp Leu Pro Val Ser
135             100                 105                 110
136 Asn Asp Pro Asp Asn Pro Cys Ser Leu Lys Cys Gln Ala Lys Gly Thr
137         115                 120                 125
138 Thr Leu Val Val Glu Leu Ala Pro Lys Val Leu Asp Gly Thr Arg Cys
139     130                 135                 140
140 Tyr Thr Glu Ser Leu Asp Met Cys Ile Ser Gly Leu Cys Gln Ile Val
141 145                 150                 155                 160
142 Gly Cys Asp His Gln Leu Gly Ser Thr Val Lys Glu Asp Asn Cys Gly
143                 165                 170                 175
144 Val Cys Asn Gly Asp Gly Ser Thr Cys Arg Leu Val Arg Gly Gln Tyr
145             180                 185                 190
146 Lys Ser Gln Leu Ser Ala Thr Lys Ser Asp Asp Thr Val Val Ala Ile
147         195                 200                 205
148 Pro Tyr Gly Ser Arg His Ile Arg Leu Val Leu Lys Gly Pro Asp His
149     210                 215                 220
150 Leu Tyr Leu Glu Thr Lys Thr Leu Gln Gly Thr Lys Gly Glu Asn Ser
151 225                 230                 235                 240
152 Leu Ser Ser Thr Gly Thr Phe Leu Val Asp Asn Ser Ser Val Asp Phe
153                 245                 250                 255
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157         275                 280                 285
158 Val Gln Phe Ile Phe Tyr Gln Pro Ile Ile His Arg Trp Arg Glu Thr
159     290                 295                 300
160 Asp Phe Phe Pro Cys Ser Ala Thr Cys Gly Gly Gly Tyr Gln Leu Thr
161 305                 310                 315                 320
162 Ser Ala Glu Cys Tyr Asp Leu Arg Ser Asn Arg Val Val Ala Asp Gln
163                 325                 330                 335
164 Tyr Cys His Tyr Tyr Pro Glu Asn Ile Lys Pro Lys Pro Lys Leu Gln
165             340                 345                 350
166 Glu Cys Asn Leu Asp Pro Cys Pro Ala Ser Asp Gly Tyr Lys Gln Ile
167         355                 360                 365
168 Met Pro Tyr Asp Leu Tyr His Pro Leu Pro Arg Trp Glu Ala Thr Pro
169     370                 375                 380
170 Trp Thr Ala Cys Ser Ser Ser Cys Gly Gly Gly Ile Gln Ser Arg Ala
171 385                 390                 395                 400
172 Val Ser Cys Val Glu Glu Asp Ile Gln Gly His Val Thr Ser Val Glu
173                 405                 410                 415
174 Glu Trp Lys Cys Met Tyr Thr Pro Lys Met Pro Ile Ala Gln Pro Cys
175             420                 425                 430
176 Asn Ile Phe Asp Cys Pro Lys Trp Leu Ala Gln Glu Trp Ser Pro Cys
177         435                 440                 445
178 Thr Val Thr Cys Gly Gln Gly Leu Arg Tyr Arg Val Val Leu Cys Ile
179     450                 455                 460
180 Asp His Arg Gly Met His Thr Gly Gly Cys Ser Pro Lys Thr Lys Pro
181 465                 470                 475                 480
182 His Ile Lys Glu Glu Cys Ile Val Pro Thr Pro Cys Tyr Lys Pro Lys
183                 485                 490                 495
184 Glu Lys Leu Pro Val Glu Ala Lys Leu Pro Trp Phe Lys Gln Ala Gln
185             500                 505                 510
186 Glu Leu Glu Glu Gly Ala Ala Val Ser Glu Glu Pro Ser Phe Ile Pro
187         515                 520                 525
188 Glu Ala Trp Ser Ala Cys Thr Val Thr Cys Gly Val Gly Thr Gln Val
189     530                 535                 540
190 Arg Ile Val Arg Cys Gln Val Leu Leu Ser Phe Ser Gln Ser Val Ala
191 545                 550                 555                 560
192 Asp Leu Pro Ile Asp Glu Cys Glu Gly Pro Lys Pro Ala Ser Gln Arg
193                 565                 570                 575
194 Ala Cys Tyr Ala Gly Pro Cys Ser Gly Glu Ile Pro Glu Phe Asn Pro
195             580                 585                 590
196 Asp Glu Thr Asp Gly Leu Phe Gly Gly Leu Gln Asp Phe Asp Glu Leu
197         595                 600                 605
198 Tyr Asp Trp Glu Tyr Glu Gly Phe Thr Lys Cys Ser Glu Ser Cys Gly
199     610                 615                 620
200 Gly Gly Val Gln Glu Ala Val Val Ser Cys Leu Asn Lys Gln Thr Arg
201 625                 630                 635                 640
202 Glu Pro Ala Glu Glu Asn Leu Cys Val Thr Ser Arg Arg Pro Pro Gln
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204 Leu Leu Lys Ser Cys Asn Leu Asp Pro Cys Pro Ala Arg Trp Glu Ile
205             660                 665                 670
206 Gly Lys Trp Ser Pro Cys Ser Leu Thr Cys Gly Val Gly Leu Gln Thr
207         675                 680                 685
208 Arg Asp Val Phe Cys Ser His Leu Leu Ser Arg Glu Met Asn Glu Thr
209     690                 695                 700
210 Val Ile Leu Ala Asp Glu Leu Cys Arg Gln Pro Lys Pro Ser Thr Val
211 705                 710                 715                 720
212 Gln Ala Cys Asn Arg Phe Asn Cys Pro Pro Ala Trp Tyr Pro Ala Gln
213                 725                 730                 735
214 Trp Gln Pro Cys Ser Arg Thr Cys Gly Gly Gly Val Gln Lys Arg Glu
215             740                 745                 750
216 Val Leu Cys Lys Gln Arg Met Ala Asp Gly Ser Phe Leu Glu Leu Pro
217         755                 760                 765
218 Glu Thr Phe Cys Ser Ala Ser Lys Pro Ala Cys Gln Gln Ala Cys Lys
219     770                 775                 780
220 Lys Asp Asp Cys Pro Ser Glu Trp Leu Leu Ser Asp Trp Thr Glu Cys
221 785                 790                 795                 800
222 Ser Thr Ser Cys Gly Glu Gly Thr Gln Thr Arg Ser Ala Ile Cys Arg
223                 805                 810                 815
224 Lys Met Leu Lys Thr Gly Leu Ser Thr Val Val Asn Ser Thr Leu Cys
225             820                 825                 830
226 Pro Pro Leu Pro Phe Ser Ser Ser Ile Arg Pro Cys Met Leu Ala Thr
227         835                 840                 845
228 Cys Ala Arg Pro Gly Arg Pro Ser Thr Lys His Ser Pro His Ile Ala
229     850                 855                 860
230 Ala Ala Arg Lys Val Tyr Ile Gln Thr Arg Arg Gln Arg Lys Leu His
231 865                 870                 875                 880
232 Phe Val Val Gly Gly Phe Ala Tyr Leu Leu Pro Lys Thr Ala Val Val
233                 885                 890                 895
234 Leu Arg Cys Pro Ala Arg Arg Val Arg Lys Pro Leu Ile Thr Trp Glu
235             900                 905                 910
236 Lys Asp Gly Gln His Leu Ile Ser Ser Thr His Val Thr Val Ala Pro
237         915                 920                 925
238 Phe Gly Tyr Leu Lys Ile His Arg Leu Lys Pro Ser Asp Ala Gly Val
239     930                 935                 940
240 Tyr Thr Cys Ser Ala Gly Pro Ala Arg Glu His Phe Val Ile Lys Leu
241 945                 950                 955                 960
242 Ile Gly Gly Asn Arg Lys Leu Val Ala Arg Pro Leu Ser Pro Arg Ser
243                 965                 970                 975
244 Glu Glu Glu Val Leu Ala Gly Arg Lys Gly Gly Pro Lys Glu Ala Leu
245             980                 985                 990
246 Gln Thr His Lys His Gln Asn Gly Ile Phe Ser Asn Gly Ser Lys Ala
247         995                 1000                1005
248 Glu Lys Arg Gly Leu Ala Ala Asn Pro Gly Ser Arg Tyr Asp Asp Leu
249     1010                1015                1020
250 Val Ser Arg Leu Leu Glu Gln Gly Gly Trp Pro Gly Glu Leu Leu Ala
251 1025                1030                1035                1040
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VERIFICATION SUMMARY DATE: 01/30/2002
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L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date